

**BLAST Search Results**

BLAST Entrez ?

09/44,242
Attach Paper #7

BLASTP 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 979256398-29007-2583

Query= gi|10059694|gb|AAE36324.1| Sequence 2 from patent US
5985598

(113 letters)

Database: Non-redundant SwissProt sequences
91,096 sequences; 32,794,363 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 10 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:		Score (bits)	E Value
sp P56279 TCLA HUMAN	T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P...	203	1e-52
sp P56280 TCLA MOUSE	T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P...	104	6e-23
sp P56278 MTC2 HUMAN	P13 MTCP-1 PROTEIN (MATURE T-CELL PROL...	78	6e-15
sp Q60945 MTC2 MOUSE	P13 MTCP-1 PROTEIN (MATURE T-CELL PROL...	76	2e-14
sp O95988 TCLB HUMAN	T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1B (T...	56	3e-08
sp P56845 TLB5 MOUSE	TCL1B5 PROTEIN	39	0.005
sp P56844 TLB4 MOUSE	TCL1B4 PROTEIN	38	0.007
sp P56842 TLB3 MOUSE	TCL1B3 PROTEIN	35	0.046
sp P56840 TLB1 MOUSE	TCL1B1 PROTEIN	35	0.079
sp P56841 TLB2 MOUSE	TCL1B2 PROTEIN	35	0.079

Alignments

>sp|P56279|TCLA HUMAN T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P14 TCL1 PROTEIN) (TCL1 ONCOGENE) (TCL-1 PROTEIN)
Length = 114

Score = 203 bits (516), Expect = 1e-52
Identities = 96/113 (84%), Positives = 96/113 (84%)

Query: 1 AECPTLGEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXXXXP 60
AECPTLGEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKD P
Sbjct: 2 AECPTLGEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGRP 61

Query: 61 MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLYHIKIDGVEDMLLELLPDD 113
MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLYHIKIDGVEDMLLELLPDD
Sbjct: 62 MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLYHIKIDGVEDMLLELLPDD 114

>sp|P56280|TCLA MOUSE T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P14 TCL1 PROTEIN) (TCL1 ONCOGENE) (TCL-1 PROTEIN)
Length = 116

Score = 104 bits (260), Expect = 6e-23
Identities = 49/101 (48%), Positives = 63/101 (61%), Gaps = 2/101 (1%)

Query: 13 HPDRLWAWKEFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXXXXPMTPTQIGPSLLP 72
HP+RLW WEK VYLDE + +WLP+ I K M+P+Q+ P LP
Sbjct: 14 HPNRLWIWEKHVYLDEFRRSWLPVVI--KSNEKFQVILRQEDVTLGAMSPSQLVPYELP 71

Query: 73 IMWQLYPDGRYRSSDSSFWRVLYHIKIDGVEDMLLELLPDD 113
+MWQLYP RYRS DS +W+++YHIK VEDMLLEL+ +
Sbjct: 72 LMWQLYPKDRYRSCDSMYQILYHIKFRDVEDMLLELIDSE 112

>sp|P56278|MTC2 HUMAN P13 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE B1) (MT TYPE B1) (P13MTCP1)
Length = 107

Score = 78.2 bits (191), Expect = 6e-15
Identities = 37/107 (34%), Positives = 58/107 (53%), Gaps = 2/107 (1%)

Query: 7 GEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXXXXPMTPTQI 66
GE V PD LW ++ +Y DE Q W+ + E + P+ +
Sbjct: 3 GEDVGAPPDHLWVHQEGIYRDEYQRTWVAVVEE--ETSFLRARVQIQVPLGDAARPSHL 60

Query: 67 GPSLLPIMWQLYPDGRYRSSDSSFWRVLYHIKIDGVEDMLLELLPDD 113
S LP+MWQLYP+ RY ++S W++ +H+ + GV+++LL+LLPDD
Sbjct: 61 LTSQLPLMWQLYPEERYMDNNSRLWQIQHMLMVRGVQELLLKLLPDD 107

>sp|Q60945|MTC2 MOUSE P13 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE B1) (MT TYPE B1) (P13MTCP1)
Length = 107

Score = 76.3 bits (186), Expect = 2e-14
Identities = 37/106 (34%), Positives = 57/106 (52%), Gaps = 2/106 (1%)

Query: 8 EAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXXXXPMTPTQIG 67
E V PD LW ++ VY DE Q W+ + E + P+ +
Sbjct: 4 EDVGAPPDHLWVHQEGVYRDEYQRTWVAVVEE--ETSFLKARVQVQVPLGDATKPSHLL 61

Query: 68 PSLLPIMWQLYPDGRYRSSDSSFWRVLYHIKIDGVEDMLLELLPDD 113
S LP+MWQLYP+ RY ++S W++ +H+ + GV+++LL+LLPDD
Sbjct: 62 TSQLPLMWQLYPEERYMDNNSRLWQIQHMLMVRGVQELLLKLLPDD 107

>sp|O95988|TCLB HUMAN T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1B (TCL1B ONCOGENE) (SYNCYTIOTROPHOBLAST-SPECIFIC PROTEIN) (SYN-1)

Length = 128

Score = 55.8 bits (133), Expect = 3e-08

Identities = 30/113 (26%), Positives = 48/113 (41%), Gaps = 14/113 (12%)

Query: 14 PDRLWAWKEFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXX-----XXX 59
 P RLW +Y DE+ W+ + +

Sbjct: 13 PGRLWIQRPGIYEDEEGRTWVTVVVRFNPSRREWARASQGSRYEPSITVHLWQMAVHTRE 72

Query: 60 PMTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLELLPD 112
 ++ Q+ S LP +WQLYP +YR++DSSFW + H +ID +E ++L P+

Sbjct: 73 LLSSGQMPFSQLPAVWQLYPGRKYAADSSFWIADHGQIDSMEQLVLTYQPE 125

>sp|P56845|TLB5 MOUSE TCL1B5 PROTEIN

Length = 121

Score = 38.5 bits (88), Expect = 0.005

Identities = 21/94 (22%), Positives = 37/94 (39%), Gaps = 7/94 (7%)

Query: 24 VYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXX---XXXPMTPTQIGP---SLLPIMWQ 76
 +Y DE W+ + +E P PT P + LP MW+

Sbjct: 23 IYEDEHHRVWIAVNVETSHSSHGNRIETCVTVHLQHMTTLPQEPTPQQPINNNSLPTMWR 82

Query: 77 LYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLELL 110
 L Y +D ++WRL+ H ++ + L+++

Sbjct: 83 LESRNTYTGTDTGYWRLLDHSQMGDTVQLTLDII 116

>sp|P56844|TLB4 MOUSE TCL1B4 PROTEIN

Length = 120

Score = 38.1 bits (87), Expect = 0.007

Identities = 25/94 (26%), Positives = 35/94 (36%), Gaps = 8/94 (8%)

Query: 24 VYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXPMTPTQIGPS-----LLPIMW 75
 +Y DE W+ +E MT PS LP W

Sbjct: 24 IYEDEHGRQWAAKVETSSHSPIYSKIETCVTVHLWQMTTLFQEPSPDSLKTFNFLPTW 83

Query: 76 QLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLEL 109
 +L YR +D+ WRLV H + G E+++L L

Sbjct: 84 RLESNTYRGADAMHWRLVNHSQFYGTEELVLML 117

>sp|P56842|TLB3 MOUSE TCL1B3 PROTEIN

Length = 122

Score = 35.4 bits (80), Expect = 0.046

Identities = 16/50 (32%), Positives = 29/50 (58%), Gaps = 1/50 (2%)

Query: 62 TPTQ-IGPSLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLELL 110
 TP Q I + LP MW+L Y +D ++WRL+ H ++ ++L+++

Sbjct: 68 TPQQPINNNSLPTMWRLESMNTYTGTDTGYWRLLDHSQMGDTLQLILDIV 117

>sp|P56840|TLB1 MOUSE TCL1B1 PROTEIN

Length = 116

Score = 34.7 bits (78), Expect = 0.079

Identities = 21/93 (22%), Positives = 36/93 (38%), Gaps = 7/93 (7%)

Query: 24 VYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXPMTPTQIGP-----SLLPIMWQL 77
 +Y DE W+ +E + P Q+ P LP W+L

Sbjct: 23 IYEDEHHRVWIVANVETSHSSHGNRRRTHVTVHLWK-LIPQQVIPFNPLNYDFLPTTWKL 81

Query: 78 YPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLELL 110
 Y ++D + WRL+ H ++ E ++L L+

Sbjct: 82 ESRNIYWATDGTWRLLDHSQLGDTQLILMLV 114

>sp|P56841|TLB2 MOUSE TCL1B2 PROTEIN
Length = 117

Score = 34.7 bits (78), Expect = 0.079
Identities = 16/53 (30%), Positives = 26/53 (48%), Gaps = 3/53 (5%)

Query: 60 PMTPTQIGP---SLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLLEL 109
P P P + LP+ W+L YR +D+ WRL+ H ++ ++L L
Sbjct: 64 PQEPAPYNPMNYNFLPMTWRLLASMTYRGTDAMHWRLNHSQVGDTVQLILML 116

Database: Non-redundant SwissProt sequences
Posted date: Jan 9, 2001 10:09 PM
Number of letters in database: 32,794,363
Number of sequences in database: 91,096

Lambda	K	H
0.320	0.141	0.473

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 7307966
Number of Sequences: 91096
Number of extensions: 223494
Number of successful extensions: 369
Number of sequences better than 10.0: 10
Number of HSP's better than 10.0 without gapping: 10
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 354
Number of HSP's gapped (non-prelim): 10
length of query: 113
length of database: 32,794,363
effective HSP length: 40
effective length of query: 73
effective length of database: 29,150,523
effective search space: 2127988179
effective search space used: 2127988179
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 60 (27.7 bits)



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search <input type="text" value="Protein"/>		<input checked="" type="checkbox"/> for				<input type="button" value="Go"/>	<input type="button" value="Clear"/>
		<input type="button" value="Limits"/>	<input type="button" value="Index"/>	<input type="button" value="History"/>	<input type="button" value="Clipboard"/>		
<input type="button" value="Display"/>	<input type="button" value="Default View"/>	<input checked="" type="checkbox"/> as	<input type="button" value="HTML"/>	<input checked="" type="checkbox"/>	<input type="button" value="Save"/>	<input type="button" value="Add to Clipboard"/>	<input type="button" value="Hide Brief and LinkB"/>

☐ 1: GI "3024700" [GenPept] T-CELL LEUKEMIA/LYMPHOMA PR... BLink, PubMed, Related Seq

LOCUS TCLA_MOUSE 116 aa ROD 30-MAY-2000
 DEFINITION T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P14 TCL1 PROTEIN) (TCL1 ONCOGENE) (TCL-1 PROTEIN).
 ACCESSION P56280
 PID g3024700
 VERSION P56280 GI:3024700
 DBSOURCE swissprot: locus TCLA_MOUSE, accession* P56280;
 class: standard.
 created: Jul 15, 1998.
 sequence updated: Jul 15, 1998.
 annotation updated: May 30, 2000.
 xrefs: gi: gi: 2645693, gi: gi: 2645694, gi: gi: 2597985, gi: gi: 2597986
 xrefs (non-sequence databases): HSSP P56279, MGD MGI:1097166, PFAM PF01840
 KEYWORDS Microsome.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 116)
 AUTHORS Narducci, M.G., Virgilio, L., Engiles, J.B., Buchberg, A.M., Billips, L., Facchiano, A., Croce, C.M., Russo, G. and Rothstein, J.L.
 TITLE The murine Tc11 oncogene: embryonic and lymphoid cell expression
 JOURNAL Oncogene 15 (8), 919-926 (1997)
 MEDLINE 97430049
 REMARK SEQUENCE FROM N.A.
 COMMENT

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[SUBCELLULAR LOCATION] MICROSOMAL FRACTION (BY SIMILARITY).
 [SIMILARITY] BELONGS TO THE TCL1 FAMILY.

FEATURES Location/Qualifiers
 source 1..116
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 1..116
 Protein 1..116
 /product="T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A"

ORIGIN
 1 matqrahrae tpahpnrlwi wekhvyldef rrswlppvik snekfqvilr qedvtlgeam
 61 spsqlypyel plmwqlypkd ryrscdsmyw qilyhikfrd vedmllelid sesnde
 //

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search <input type="text" value="Protein"/>		<input checked="" type="checkbox"/> for				<input type="button" value="Go"/>	<input type="button" value="Clear"/>
		<input type="button" value="Limits"/>	<input type="button" value="Index"/>	<input type="button" value="History"/>	<input type="button" value="Clipboard"/>		
<input type="button" value="Display"/>	<input type="button" value="Default View"/>	<input checked="" type="checkbox"/> as	<input type="button" value="HTML"/>	<input checked="" type="checkbox"/>	<input type="button" value="Save"/>	<input type="button" value="Add to Clipboard"/>	<input type="button" value="Hide Brief and LinkB"/>

☐ 1: GI "3024175" [GenPept] P13 MTCP-1 PROTEIN (MATURE ... BLINK, PubMed, Related Sequer

LOCUS MTC2_HUMAN 107 aa PRI 30-MAY-2000
 DEFINITION P13 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE B1) (MTCP-1 TYPE B1) (P13MTCP1).
 ACCESSION P56278
 PID g3024175
 VERSION P56278 GI:3024175
 DBSOURCE swissprot: locus MTC2_HUMAN, accession P56278;
 class: standard.
 created: Jul 15, 1998.
 sequence updated: Jul 15, 1998.
 annotation updated: May 30, 2000.
 xrefs: gi: gi: 2252491, gi: gi: 2252492, gi: gi: 3212251
 xrefs (non-sequence databases): MIM 300116, PFAM PF01840
 KEYWORDS Proto-oncogene; Chromosomal translocation; Alternative splicing;
 3D-structure.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 107)
 AUTHORS Stern,M.H., Soulier,J., Rosenzweig,M., Nakahara,K., Canki-Klain,N.,
 Aurias,A., Sigaux,F. and Kirsch,I.R.
 TITLE MTCP-1: a novel gene on the human chromosome Xq28 translocated to
 the T cell receptor alpha/delta locus in mature T cell
 proliferations
 JOURNAL Oncogene 8 (9), 2475-2483 (1993)
 MEDLINE 93368950
 REMARK SEQUENCE FROM N.A.
 TISSUE=T-CELL
 REFERENCE 2 (residues 1 to 107)
 AUTHORS Fu,Z.Q., Du Bois,G.C., Song,S.P., Kulikovskaya,I., Virgilio,L.,
 Rothstein,J.L., Croce,C.M., Weber,I.T. and Harrison,R.W.
 TITLE Crystal structure of MTCP-1: implications for role of TCL-1 and
 MTCP-1 in T cell malignancies
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3413-3418 (1998)
 MEDLINE 98188217
 REMARK X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 COMMENT

 This SWISS-PROT entry is copyright. It is produced through a
 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[ALTERNATIVE PRODUCTS] ALTERNATIVE SPLICING PRODUCES TWO SHORT, YET
 COMPLETELY DIFFERENT PROTEINS. THE LONGER PRODUCT, TYPE-B1, IS
 KNOWN AS P13 MTCP-1 (AC P56278). THE SHORTER PRODUCT, TYPE-A, IS

KNOWN AS P8 MTCP-1 (AC P56277).
[TISSUE SPECIFICITY] NOT FOUND AT A SIGNIFICANT LEVEL IN ANY
TISSUE.
[DISEASE] DETECTED IN T-CELL LEUKEMIA BEARING A T(X;14)
TRANSLOCATION. PLAYS A KEY ROLE IN T-CELL PROLYMPHOCYTIC LEUKEMIA.
[SIMILARITY] BELONGS TO THE TCL1 FAMILY.

FEATURES Location/Qualifiers
 source 1..107
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..107
 Protein 1..107
 /product="P13 MTCP-1 PROTEIN"

ORIGIN
 1 magedvgapp dhlwvhqegi yrdeyqrtwv avveetsfl rarvqqiqvp lgdaarpshl
 61 ltsqlplmwq lypeerymdn nsrlwqiqhh lmvgvqell lkllpdd
//

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Limits		Preview/Index		History		Clipboard		

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Entrez PubMed

☐ 1: *Oncogene* 1993
Sep;8(9):2475-83

Related Articles, Books, Protein, Nucleotide,
Structure, Genome, OMIM, LinkOut

PubMed Services

**MTCP-1: a novel gene on the human chromosome Xq28
translocated to the T cell receptor alpha/delta locus in mature
T cell proliferations.**

**Stern MH, Soulier J, Rosenzweig M, Nakahara K, Canki-Klain N,
Aurias A, Sigaux F, Kirsch IR**

Related Resources

Laboratoire d'Hematologie Moleculaire, Hopital Saint-Louis, Paris, France.

T-cell lymphoproliferative diseases are often associated with recurrent chromosomal translocations involving T cell receptor genes (TCR) and genes that are thought to play a role in the pathogenesis of these diseases. Whereas numerous such genes have already been identified in acute T cell leukemias, no candidate gene has yet been identified to play a role in the heterogeneous group of T cell proliferations with a mature phenotype. We here report the molecular cloning of two examples of the rare but recurrent t(X;14) translocation. The first translocation was associated with a benign clonal proliferation in an ataxia telangiectasia patient and the second with a T cell prolymphocytic leukemia. Both translocations implicated the TCR alpha/delta locus and a common breakpoint region on chromosome Xq28. A previously unidentified gene, abnormally transcribed in both T cell proliferations, was characterized in the immediate proximity of the breakpoints. This Xq28 gene has no homology with known sequences, uses a complex alternative splicing pattern and demonstrates two short open reading frames. This gene, named MTCP-1 (Mature T Cell Proliferation-1) is the first candidate gene potentially involved in the leukemogenic process of mature T cell proliferations.

MeSH Terms:

- Alternative Splicing
- Amino Acid Sequence
- Ataxia Telangiectasia/genetics
- Base Sequence
- Chromosomes, Human, Pair 14
- Gene Expression

- Genes, Structural
- Human
- Leukemia, Prolymphocytic/genetics
- Lymphoproliferative Disorders/genetics*
- Molecular Sequence Data
- Proto-Oncogene Proteins/genetics*
- Receptors, Antigen, T-Cell, alpha-beta/genetics*
- Restriction Mapping
- RNA, Messenger/genetics
- Support, Non-U.S. Gov't
- T-Lymphocytes/cytology
- Translocation (Genetics)*
- X Chromosome*

Gene Symbols:

- MTCP-1

Substances:

- RNA, Messenger
- Receptors, Antigen, T-Cell, alpha-beta
- Proto-Oncogene Proteins
- MTCP-1 protein

PMID: 8361760, UI: 93368950

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[Department of Health & Human Services](#)
[Freedom of Information Act](#) | [Disclaimer](#)



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Search		Protein	for				Go Clear
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Display	Default View	as	HTML	Save	Add to Clipboard	Hide Brief and LinkB	

☐ 1: GI "2498592" [GenPept] P13 MTCP-1 PROTEIN (MATURE ... BLink, PubMed, Related Sequer

LOCUS MTC2_MOUSE 107 aa ROD 30-MAY-2000
 DEFINITION P13 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE B1) (MTCP-1 TYPE B1) (P13MTCP1).
 ACCESSION Q60945
 PID g2498592
 VERSION Q60945 GI:2498592
 DBSOURCE swissprot: locus MTC2_MOUSE, accession Q60945;
 class: standard.
 created: Nov 1, 1997.
 sequence updated: Nov 1, 1997.
 annotation updated: May 30, 2000.
 xrefs: gi: gi: 1229159, gi: gi: 1229160
 xrefs (non-sequence databases): HSSP P56278, MGD MGI:102699, PFAM PF01840
 KEYWORDS Alternative splicing.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 107)
 AUTHORS Madani,A., Choukroun,V., Soulier,J., Cacheux,V., Claisse,J.-F.,
 Valensi,F., Daliphard,S., Cazin,B., Levy,V., Leblond,V.,
 Daniel,M.-T., Sigaux,F. and Stern,M.-H.
 TITLE Expression of p13MTCP1 is restricted to mature T-cell
 proliferations with t(X;14) translocations
 JOURNAL Blood 87 (5), 1923-1927 (1996)
 MEDLINE 96202516
 REMARK SEQUENCE FROM N.A.
 TISSUE=T-CELL

COMMENT -----
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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[ALTERNATIVE PRODUCTS] ALTERNATIVE SPLICING PRODUCES TWO SHORT, YET
 COMPLETELY DIFFERENT PROTEINS. THE LONGER PRODUCT, TYPE-B1, IS
 KNOWN AS P13 MTCP-1 (AC Q60945). THE SHORTER PRODUCT, TYPE-A, IS
 KNOWN AS P8 MTCP-1 (AC Q61908).

[TISSUE SPECIFICITY] NOT FOUND AT A SIGNIFICANT LEVEL IN ANY
 TISSUE.

[SIMILARITY] BELONGS TO THE TCL1 FAMILY.

FEATURES Location/Qualifiers
 source 1..107
 /organism="Mus musculus"
 /db_xref="taxon:10090"

Protein 1..107
1..107
/product="P13 MTCP-1 PROTEIN"
ORIGIN
1 maredvgapp dhlwvhqegv yrdeyqrtwv avveetsfl karvqqvqvp lgdatkpshl
61 ltsqlplmwq lypeerymdn nsrlwqiqhh lmvrqvqell lklpdd
//

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Search		Protein	for				Go Clear
		Limits	Index	History	Clipboard		
Display	Default View	as	HTML	Save	Add to Clipboard	Hide Brief and LinkB	

☐ 1: GI "6831692" [GenPept] T-CELL LEUKEMIA/LYMPHOMA PR... BLink, PubMed, Related Sec

LOCUS TCLB HUMAN 128 aa PRI 30-MAY-2000
 DEFINITION T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1B (TCL1B ONCOGENE)
 (SYNCYTIOTROPHOBLAST-SPECIFIC PROTEIN) (SYN-1).
 ACCESSION O95988
 PID g6831692
 VERSION O95988 GI:6831692
 DBSOURCE swissprot: locus TCLB_HUMAN, accession O95988;
 class: standard.
 created: May 30, 2000.
 sequence updated: May 30, 2000.
 annotation updated: May 30, 2000.
 xrefs: gi: gi: 4324704, gi: gi: 4324705, gi: gi: 4324702, gi: gi:
 4324703, gi: gi: 4809182, gi: gi: 4809183
 xrefs (non-sequence databases): HSSP P56278, MIM 603769
 KEYWORDS Proto-oncogene; Chromosomal translocation.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 128)
 AUTHORS Pekarsky,Y., Hallas,C., Isobe,M., Russo,G. and Croce,C.M.
 TITLE Abnormalities at 14q32.1 in T cell malignancies involve two
 oncogenes
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2949-2951 (1999)
 MEDLINE 99178995
 REMARK SEQUENCE FROM N.A.
 REFERENCE 2 (residues 1 to 128)
 AUTHORS Jiang,B. and Mendelson,C.R.
 TITLE Direct Submission
 JOURNAL Submitted (??-MAR-1999)
 REMARK SEQUENCE FROM N.A.

COMMENT

 This SWISS-PROT entry is copyright. It is produced through a
 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[TISSUE SPECIFICITY] EXPRESSED IN A VARIETY OF TISSUES.
 [DISEASE] ACTIVATED IN CHRONIC T-CELL LEUKEMIAS (T-CLL) CARRYING
 REARRANGEMENTS OF THE 14Q32.1 REGION.
 [SIMILARITY] BELONGS TO THE TCL1 FAMILY.

FEATURES
 source Location/Qualifiers
 1..128
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..128

Protein

1..128

/product="T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1B"

ORIGIN

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1 maseasvrlg vppgrlwiqr pgiyedeegr twvtvvvrfn psrrewaras qgsryepsit
61 vhlwqmvavht relssgqmp fsqlpavwql ypgrkyraad ssfweiadhg qidsmeqlvl
121 tyqperkd
```

//

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**BLAST Search Results**

BLAST Entrez ?

BLASTP 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 979256332-27868-28584

Query= gi|10059694|gb|AAE36324.1| Sequence 2 from patent US 5985598
(113 letters)

Database: pat

58,877 sequences; 7,873,053 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 2 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gb|AAE36324.1| Sequence 2 from patent US 5985598
gb|AAE36325.1| Sequence 4 from patent US 5985598

203 3e-53
78 1e-15

Alignments

>gb|AAE36324.1| Sequence 2 from patent US 5985598
Length = 113

Score = 203 bits (516), Expect = 3e-53
Identities = 96/113 (84%), Positives = 96/113 (84%)

Query: 1 AECPTLGEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXXXXP 60
AECPTLGEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKD P
Sbjct: 1 AECPTLGEAVTDHPDRLWAWKEFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGRP 60

Query: 61 MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLELLPDD 113
 MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLELLPDD
 Sbjct: 61 MTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLELLPDD 113

>gb|AAE36325.1| Sequence 4 from patent US 5985598
 Length = 108

Score = 78.2 bits (191), Expect = 1e-15
 Identities = 37/107 (34%), Positives = 58/107 (53%), Gaps = 2/107 (1%)

Query: 7 GEAVTDHPDRLWAWKEKFVYLDEKQHAWLPLTIEIKDXXXXXXXXXXXXXXXXXPMPTPTQI 66
 GE V PD LW ++ +Y DE Q W+ + E + P+ +
 Sbjct: 3 GEDVGAPPDHLWVHQEGIYRDEYQRTWVAVVEE--ETSFLRARVQQIQVPLGDAARPSHL 60

Query: 67 GPSLLPIMWQLYPDGRYRSSDSSFWRVLVYHIKIDGVEDMLELLPDD 113
 S LP+MWQLYP+ RY ++S W++ +H+ + GV+++LL+LLPDD
 Sbjct: 61 LTSQLPLMWQLYPEERYMDNNSRLWQIQHHLMVVRGVQELLLKLLPDD 107

Database: pat
 Posted date: Jan 10, 2001 9:47 PM
 Number of letters in database: 7,873,053
 Number of sequences in database: 58,877

Lambda	K	H
0.320	0.141	0.473

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 1804225
 Number of Sequences: 58877
 Number of extensions: 53218
 Number of successful extensions: 109
 Number of sequences better than 10.0: 2
 Number of HSP's better than 10.0 without gapping: 2
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 105
 Number of HSP's gapped (non-prelim): 2
 length of query: 113
 length of database: 7,873,053
 effective HSP length: 35
 effective length of query: 78
 effective length of database: 5,812,358
 effective search space: 453363924
 effective search space used: 453363924
 T: 11
 A: 40
 X1: 16 (7.4 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (21.8 bits)
 S2: 55 (25.8 bits)



Protein

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	<input checked="" type="checkbox"/> for				Go	Clear
Limits		Index		History		Clipboard	
Display	Default View	<input checked="" type="checkbox"/> as	HTML	<input checked="" type="checkbox"/> Save	Add to Clipboard	<input type="checkbox"/> Hide Brief and LinkB	

☐ 1: GI "3024699" [GenPept] T-CELL LEUKEMIA/LYMPHOMA PR... BLink, PubMed, Related Ser

LOCUS TCLA_HUMAN 114 aa PRI 30-MAY-2000
 DEFINITION T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A (P14 TCL1 PROTEIN) (TCL1 ONCOGENE) (TCL-1 PROTEIN).
 ACCESSION P56279
 PID g3024699
 VERSION P56279 GI:3024699
 DBSOURCE swissprot: locus TCLA_HUMAN, accession P56279;
 class: standard.
 created: Jul 15, 1998.
 sequence updated: Jul 15, 1998.
 annotation updated: May 30, 2000.
 xrefs: gi: gi: 624960, gi: gi: 624961, gi: gi: 2981785
 xrefs (non-sequence databases): MIM 186960, PFAM PF01840
 KEYWORDS Proto-oncogene; Chromosomal translocation; Microsome; 3D-structure.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 114)
 AUTHORS Virgilio,L., Narducci,M.G., Isobe,M., Billips,L.G., Cooper,M.D., Croce,C.M. and Russo,G.
 TITLE Identification of the TCL1 gene involved in T-cell malignancies
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (26), 12530-12534 (1994)
 MEDLINE 95107991
 REMARK SEQUENCE FROM N.A.
 REFERENCE 2 (residues 1 to 114)
 AUTHORS Fu,T.B., Virgilio,L., Narducci,M.G., Facchiano,A., Russo,G. and Croce,C.M.
 TITLE Characterization and localization of the TCL-1 oncogene product
 JOURNAL Cancer Res. 54 (24), 6297-6301 (1994)
 MEDLINE 95079394
 REMARK CHARACTERIZATION, AND LOCALIZATION.
 REFERENCE 3 (residues 1 to 114)
 AUTHORS Hoh,F., Yang,Y.S., Guignard,L., Padilla,A., Stern,M.H., Lhoste,J.M. and van Tilbeurgh,H.
 TITLE Crystal structure of p14TCL1, an oncogene product involved in T-cell prolymphocytic leukemia, reveals a novel beta-barrel topology
 JOURNAL Structure 6 (2), 147-155 (1998)
 MEDLINE 98179932
 REMARK X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 COMMENT

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

Both
published
12/94

[SUBUNIT] HOMODIMER.
[SUBCELLULAR LOCATION] MICROSOMAL FRACTION.
[TISSUE SPECIFICITY] RESTRICTED IN THE T-CELL LINEAGE TO IMMATURE THYMOCYTES AND ACTIVATED PERIPHERAL LYMPHOCYTES. PREFERENTIALLY EXPRESSED EARLY IN T-AND B-LYMPHOCYTE DIFFERENTIATION.
[DISEASE] ACTIVATED IN CHRONIC T-CELL LEUKEMIAS (T-CLL) CARRYING T(14;14)(Q11;Q32) OR T(7;14)(Q35;Q32) CHROMOSOME TRANSLOCATIONS OR A INV(14)(Q11;Q32) CHROMOSOME INVERSION THAT INVOLVES THE T-CELL RECEPTOR ALPHA/DELTA LOCUSES.
[SIMILARITY] BELONGS TO THE TCL1 FAMILY.

FEATURES

source

Location/Qualifiers

1..114

/organism="Homo sapiens"

/db_xref="taxon:9606"

1..114

Protein

1..114

/product="T-CELL LEUKEMIA/LYMPHOMA PROTEIN 1A"

ORIGIN

1 maecptlgea vtdhpdrlwa wekfvyldk qhawlpltie ikdrlqlrvl lrredvvlgr
61 pmtptqigps llpimwqlyp dgryrssdss fwrlvyhiki dgvedmllel lpdd

//

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